Amendments to the Claims

1-43. (Canceled)

44. (Previously Presented) A method of quantifying an amount of at least a first monitor peptide and a second monitor peptide in a biological sample, comprising:

contacting the sample with

(i) a first anti-peptide antibody specific for said first peptide and;

(ii) a known quantity of a labeled version of said first peptide;

contacting the sample with

(i) a second antipeptide antibody specific for said second peptide, wherein said second antibody is different from said first antibody and;

(ii) a known quantity of a labeled version of said second peptide, separating peptides bound by said first and said second antibodies from unbound peptides;

eluting said peptides bound by said first and said second antibodies from said antibodies;

measuring the amount of said first peptide eluted from said first antibody using a mass spectrometer;

measuring the amount of said labeled version of said first peptide eluted from said first antibody using a mass spectrometer;

calculating the amount of the first peptide in the biological sample;

measuring the amount of said second peptide eluted from said second

antibody using a mass spectrometer;

measuring the amount of the labeled version of the second peptide eluted from said second antibody using a mass spectrometer; and

calculating the amount of the second peptide in the biological sample, wherein said biological sample is a proteolytic digest of a bodily fluid sample.

45-47. (Canceled)

48. (Previously Presented) The method of claim 44, wherein at least one of said first and said second antibodies is a monoclonal antibody.

49. (Previously Presented) The method of claim 44, wherein at least one of said first and said second antibodies is a polyclonal antibody.

50. (Previously Presented) The method of claim 44, wherein said first and said second antibodies are both polyclonal antibodies.

51. (Previously Presented) The method of claim 44, wherein said first and said second antibodies are both monoclonal antibodies.

52-53. (Canceled)

54. (Previously Presented) The method of claim 44, wherein the labeled version of the first peptide includes at least one site at which a stable isotope is substituted for the corresponding predominant natural isotope in more than 98% of peptide molecules.

55. (Previously Presented) The method of claim 44, further comprising: attaching the first antibody to a support.

56. (Previously Presented) The method of claim 44, further comprising: attaching the first antibody to a packed column.

57. (Previously Presented) The method of claim 44, further comprising: attaching the first antibody to a monolithic porous support.

58. (The method of claim 44, further comprising: attaching the first antibody to a mesh.

59. (Previously Presented) The method of claim 44, further comprising: attaching the first antibody to magnetic beads.

60. (Previously Presented) The method of claim 44, wherein the first peptide and the second peptide are selected from among the set of peptides produced by digestion of the target protein to provide high signal to noise in the mass spectrometer.

61. (Previously Presented) A method for quantifying the amount of a peptide, comprising:
contacting the sample with

(i) an anti-peptide antibody specific for said peptide;

(ii) a known quantity of a labeled version of the peptide,

separating peptides bound by said antibody from unbound peptides

eluting said peptide bound by said antibody from said antibody;

measuring the amount of the peptide eluted from said

antibody using a mass spectrometer: and

calculating the amount of the peptide in the biological sample;

wherein said biological sample is a proteolytic digest of a bodily fluid.

62-63. (Canceled)

64. (Previously Presented) The method of claim 61, further comprising: preparing the labeled version of the peptide.

65. (Previously Presented) The method of claim 61, wherein the labeled version of the peptide includes at least one site at which a stable isotope is substituted for the predominant natural isotope in more than 98% of peptide molecules.

66-70. (Canceled)

71. (Currently Amended) The method of claim 44 ~~67~~, further comprising:
preparing the labeled version of the monitor peptide.

72. (Currently Amended) The method of claim 71 ~~67~~, wherein the labeled version of the monitor peptide includes a stable isotope.

73. (Canceled).

74. (Previously Presented) method of claim 44, wherein said first anti-peptide antibody is created using said first peptide or a nonmaterially modified version of the first monitor peptide.

75. (Previously Presented)) The method of claim 44, further comprising: creating the first antibody using the first peptide or a non-materially modified version of the first peptide.

76. (Canceled).

77. (Previously Presented) The method of claim 61, further comprising: creating the anti-peptide antibody using the peptide or a non-materially modified version of the peptide.

78. (Currently Amended) The method of claim 44, wherein the said bound peptides are subjected to a chromatography ~~concentrating~~ step after elution from said antibodies and before introduction into said mass spectrometer.

79-80. (Canceled)

81. (Currently Amended) The method of claim 61, wherein said bound peptides are subjected to a chromatography ~~concentrating~~ step after elution from said antibody and before introduction into said mass spectrometer.

82. (Previously Presented) The method of claim 61, wherein the anti-peptide antibody is a polyclonal antibody.

83. (Previously Presented) The method of claim 61, wherein the anti-peptide antibody is a monoclonal antibody.

84. (Previously Presented) The method of claim 44 wherein said first and second peptides are proteolytically cleaved from first and second sample proteins, respectively, and wherein the amounts of said first and second proteins in said body fluid sample are calculated from the amounts of said first and said second peptides in the sample.

85. (Previously Presented) The method of claim 61 wherein said first and second peptides are proteolytically cleaved from first and second sample proteins, respectively, and wherein the amounts of said first and second proteins in said body fluid sample are calculated from the amounts of said first and said second peptides in the sample.

86. (Previously Presented) The method of claim 61, wherein the polyclonal antibody is created using the monitor peptide or a non-materially modified version of the monitor peptide.
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87. (New) The method of claim 44, wherein said first monitor peptide is a peptide fragment of TNF or IL-6.